

GM of: US-09-525-998a-11 to: SPREMBL_17:★ out_format: pfs
Date: Apr 23, 2002 10:34 PM
About: Results were produced by the GeneCore software, version 4.5.
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Command line parameters:
-MODEL=franco_nsp_model -DEV=xlp
-2 -SP=2 -USF: SP=2 -USF: SP=2 -USF: SP=2 -USF: SP=2 -USF: SP=2
-DR-SPREMBL_17 -GMI-fastan -SUFFIX-rspt -CAPOB=12,000
-GAPEXT=4,000 -MINMATCH=0.100 -LOPCL=0.000 -LOAPEXT=0.000
-QAPOP=4,500 -GAPEXT=0.050 -XGAPOP=10,000 -XGAPEXT=0.500
-FEAPOP=6,000 -DRPEXT=7,000 -YGAPOB=10,000 -YGAPEXT=0.500
-DELOP=6,000 -DRPEXT=7,000 -START=1 -MATRIX=BIOSUM62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-NRM=100 -THR_MIN=0 -ALIGN=15 -MOD=LOCAL -DIFF=0 -PFS
-USER-ext -MINLEN=0 -MAXLEN=200000000
-USER-US09525998a-11_186 -NRM=6 -ICPH=3 -LONCL=05 -NC_XLPHY
-WAIT -THREADS=1

Search information block:
Query: US-09-525-998a-11
Query length: 600
Database: SPREMBL_17:★
Database sequences: 473505
Database length: 146272129
Search time (sec): 178.770000

Score_list:	Strd	Only	ZScore	PScore	len	Document
sp_mammal:097530	+	825	50	1331	46	007530 canis familiaris (dog).
sp_mammal:095185	+	799	50	1292	30	095185 felis silvestris catus (cat).
sp_frodent:0994M1	+	296	50	457	70	0994M1 mus musculus (mouse).
sp_human:000276	-	269	50	433	57	000276 homo sapiens (human).
sp_human:000280	-	269	50	430	72	000280 homo sapiens (human).
sp_human:000275	-	269	50	430	95	000275 homo sapiens (human).
sp_vertebrate:0994V4	+	258	50	429	97	0994V4 xenopus laevis (african clawed toad).
sp_human:0949H6	+	207	50	327	32	0949H6 homo sapiens (human).
sp_human:014865	+	207	00	428	86	014865 homo sapiens (human).
sp_human:014865	+	207	00	428	86	014865 homo sapiens (human).
sp_human:0994M5	+	205	00	428	86	0994M5 homo sapiens (human).
sp_human:0994M1	+	205	00	428	73	0994M1 homo sapiens (human).
sp_frodent:0994F1	+	204	50	427	94	0994F1 mus musculus (mouse).
sp_frodent:0994F2	+	204	50	427	94	0994F2 mus musculus (mouse).
sp_frodent:0994F3	+	204	50	427	94	0994F3 mus musculus (mouse).
sp_frodent:0994F4	+	204	50	427	94	0994F4 mus musculus (mouse).
sp_frodent:0994F5	+	204	50	427	94	0994F5 mus musculus (mouse).
sp_frodent:0994F6	+	204	50	427	94	0994F6 mus musculus (mouse).
sp_frodent:0994F7	+	204	50	427	94	0994F7 mus musculus (mouse).
sp_frodent:0994F8	+	204	50	427	94	0994F8 mus musculus (mouse).
sp_frodent:0994F9	+	204	50	427	94	0994F9 mus musculus (mouse).
sp_frodent:0994F10	+	204	50	427	94	0994F10 mus musculus (mouse).
sp_frodent:0994F11	+	204	50	427	94	0994F11 mus musculus (mouse).
sp_frodent:0994F12	+	204	50	427	94	0994F12 mus musculus (mouse).
sp_frodent:0994F13	+	204	50	427	94	0994F13 mus musculus (mouse).
sp_frodent:0994F14	+	204	50	427	94	0994F14 mus musculus (mouse).
sp_frodent:0994F15	+	204	50	427	94	0994F15 mus musculus (mouse).
sp_frodent:0994F16	+	204	50	427	94	0994F16 mus musculus (mouse).
sp_frodent:0994F17	+	204	50	427	94	0994F17 mus musculus (mouse).
sp_frodent:0994F18	+	204	50	427	94	0994F18 mus musculus (mouse).
sp_frodent:0994F19	+	204	50	427	94	0994F19 mus musculus (mouse).
sp_frodent:0994F20	+	204	50	427	94	0994F20 mus musculus (mouse).
sp_frodent:0994F21	+	204	50	427	94	0994F21 mus musculus (mouse).
sp_frodent:0994F22	+	204	50	427	94	0994F22 mus musculus (mouse).
sp_frodent:0994F23	+	204	50	427	94	0994F23 mus musculus (mouse).
sp_frodent:0994F24	+	204	50	427	94	0994F24 mus musculus (mouse).
sp_frodent:0994F25	+	204	50	427	94	0994F25 mus musculus (mouse).
sp_frodent:0994F26	+	204	50	427	94	0994F26 mus musculus (mouse).
sp_frodent:0994F27	+	204	50	427	94	0994F27 mus musculus (mouse).
sp_frodent:0994F28	+	204	50	427	94	0994F28 mus musculus (mouse).
sp_frodent:0994F29	+	204	50	427	94	0994F29 mus musculus (mouse).
sp_frodent:0994F30	+	204	50	427	94	0994F30 mus musculus (mouse).
sp_frodent:0994F31	+	204	50	427	94	0994F31 mus musculus (mouse).
sp_frodent:0994F32	+	204	50	427	94	0994F32 mus musculus (mouse).
sp_frodent:0994F33	+	204	50	427	94	0994F33 mus musculus (mouse).
sp_frodent:0994F34	+	204	50	427	94	0994F34 mus musculus (mouse).
sp_frodent:0994F35	+	204	50	427	94	0994F35 mus musculus (mouse).
sp_frodent:0994F36	+	204	50	427	94	0994F36 mus musculus (mouse).
sp_frodent:0994F37	+	204	50	427	94	0994F37 mus musculus (mouse).
sp_frodent:0994F38	+	204	50	427	94	0994F38 mus musculus (mouse).
sp_frodent:0994F39	+	204	50	427	94	0994F39 mus musculus (mouse).
sp_frodent:0994F40	+	204	50	427	94	0994F40 mus musculus (mouse).
sp_frodent:0994F41	+	204	50	427	94	0994F41 mus musculus (mouse).
sp_frodent:0994F42	+	204	50	427	94	0994F42 mus musculus (mouse).
sp_frodent:0994F43	+	204	50	427	94	0994F43 mus musculus (mouse).
sp_frodent:0994F44	+	204	50	427	94	0994F44 mus musculus (mouse).
sp_frodent:0994F45	+	204	50	427	94	0994F45 mus musculus (mouse).
sp_frodent:0994F46	+	204	50	427	94	0994F46 mus musculus (mouse).
sp_frodent:0994F47	+	204	50	427	94	0994F47 mus musculus (mouse).
sp_frodent:0994F48	+	204	50	427	94	0994F48 mus musculus (mouse).
sp_frodent:0994F49	+	204	50	427	94	0994F49 mus musculus (mouse).
sp_frodent:0994F50	+	204	50	427	94	0994F50 mus musculus (mouse).
sp_frodent:0994F51	+	204	50	427	94	0994F51 mus musculus (mouse).
sp_frodent:0994F52	+	204	50	427	94	0994F52 mus musculus (mouse).
sp_frodent:0994F53	+	204	50	427	94	0994F53 mus musculus (mouse).
sp_frodent:0994F54	+	204	50	427	94	0994F54 mus musculus (mouse).
sp_frodent:0994F55	+	204	50	427	94	0994F55 mus musculus (mouse).
sp_frodent:0994F56	+	204	50	427	94	0994F56 mus musculus (mouse).
sp_frodent:0994F57	+	204	50	427	94	0994F57 mus musculus (mouse).
sp_frodent:0994F58	+	204	50	427	94	0994F58 mus musculus (mouse).
sp_frodent:0994F59	+	204	50	427	94	0994F59 mus musculus (mouse).
sp_frodent:0994F60	+	204	50	427	94	0994F60 mus musculus (mouse).
sp_frodent:0994F61	+	204	50	427	94	0994F61 mus musculus (mouse).
sp_frodent:0994F62	+	204	50	427	94	0994F62 mus musculus (mouse).
sp_frodent:0994F63	+	204	50	427	94	0994F63 mus musculus (mouse).
sp_frodent:0994F64	+	204	50	427	94	0994F64 mus musculus (mouse).
sp_frodent:0994F65	+	204	50	427	94	0994F65 mus musculus (mouse).
sp_frodent:0994F66	+	204	50	427	94	0994F66 mus musculus (mouse).
sp_frodent:0994F67	+	204	50	427	94	0994F67 mus musculus (mouse).
sp_frodent:0994F68	+	204	50	427	94	0994F68 mus musculus (mouse).
sp_frodent:0994F69	+	204	50	427	94	0994F69 mus musculus (mouse).
sp_frodent:0994F70	+	204	50	427	94	0994F70 mus musculus (mouse).
sp_frodent:0994F71	+	204	50	427	94	0994F71 mus musculus (mouse).
sp_frodent:0994F72	+	204	50	427	94	0994F72 mus musculus (mouse).
sp_frodent:0994F73	+	204	50	427	94	0994F73 mus musculus (mouse).
sp_frodent:0994F74	+	204	50	427	94	0994F74 mus musculus (mouse).
sp_frodent:0994F75	+	204	50	427	94	0994F75 mus musculus (mouse).
sp_frodent:0994F76	+	204	50	427	94	0994F76 mus musculus (mouse).
sp_frodent:0994F77	+	204	50	427	94	0994F77 mus musculus (mouse).
sp_frodent:0994F78	+	204	50	427	94	0994F78 mus musculus (mouse).
sp_frodent:0994F79	+	204	50	427	94	0994F79 mus musculus (mouse).
sp_frodent:0994F80	+	204	50	427	94	0994F80 mus musculus (mouse).
sp_frodent:0994F81	+	204	50	427	94	0994F81 mus musculus (mouse).
sp_frodent:0994F82	+	204	50	427	94	0994F82 mus musculus (mouse).
sp_frodent:0994F83	+	204	50	427	94	0994F83 mus musculus (mouse).
sp_frodent:0994F84	+	204	50	427	94	0994F84 mus musculus (mouse).
sp_frodent:0994F85	+	204	50	427	94	0994F85 mus musculus (mouse).
sp_frodent:0994F86	+	204	50	427	94	0994F86 mus musculus (mouse).
sp_frodent:0994F87	+	204	50	427	94	0994F87 mus musculus (mouse).
sp_frodent:0994F88	+	204	50	427	94	0994F88 mus musculus (mouse).
sp_frodent:0994F89	+	204	50	427	94	0994F89 mus musculus (mouse).
sp_frodent:0994F90	+	204	50	427	94	0994F90 mus musculus (mouse).
sp_frodent:0994F91	+	204	50	427	94	0994F91 mus musculus (mouse).
sp_frodent:0994F92	+	204	50	427	94	0994F92 mus musculus (mouse).
sp_frodent:0994F93	+	204	50	427	94	0994F93 mus musculus (mouse).
sp_frodent:0994F94	+	204	50	427	94	0994F94 mus musculus (mouse).
sp_frodent:0994F95	+	204	50	427	94	0994F95 mus musculus (mouse).
sp_frodent:0994F96	+	204	50	427	94	0994F96 mus musculus (mouse).
sp_frodent:0994F97	+	204	50	427	94	0994F97 mus musculus (mouse).
sp_frodent:0994F98	+	204	50	427	94	0994F98 mus musculus (mouse).
sp_frodent:0994F99	+	204	50	427	94	0994F99 mus musculus (mouse).
sp_frodent:0994F100	+	204	50	427	94	0994F100 mus musculus (mouse).

sp_virus.057100	+	167.50	263.42	057100 monkeypox virus (tupaia).
sp_virus.057101	+	167.90	263.40	057101 monkeypox virus (tupaia).
sp_virus.057102	+	167.90	263.44	057102 monkeypox virus (tupaia).
sp_virus.057103	+	167.90	261.43	057103 monkeypox virus (tupaia).
sp_virus.057104	+	166.50	261.59	057104 monkeypox virus (tupaia).
seq_name: sp_mammal:097530				
seq_documentation_block:				
AC	097530:		189 AA:	
DE	01-MAY-1999 (TrEMBLrel_10, Created)			
DT	01-MAY-1999 (TrEMBLrel_10, Last sequence update)			
DD	01-JUN-2001 (TrEMBLrel_17, Last annotation update)			
DE	TUMOR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT):			
OS	Canis familiaris (Dog)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
OX	NB1_TaxID 9515;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=BRAIN:			
RA	Bathie S., Nasir I., Argyile D.L., Ekersall P.D.			
RT	"Canine tumor necrosis factor receptor, partial cds."			
KL	Submitted (JUL 1975) to the EMBL/GenBank/DBS databases.			
EMBL	AF014955; M001516.1;			
DR	KSSP: P19438; INR:			
DR	InterPro: IPR005541; EGF-like.			
DR	InterPro: IPR003469; INFEK.			
DR	Plam: PF00020; INFEK_6;			
DR	ProDom: PD000771; INFEK_6;			
DR	SMART: SM00208; INFEK_3;			
DR	PROSITE: PS01061; EGF_2; UNKNOWN_1;			
DR	PROSITE: PS00524; INFEKFR_1;			
DR	PROSITE: PS00530; INFEKFR_2;			
FW	Receptor.			
FT	REGION: 189 189			
EQ	SEQUENCE 189 AA: 21324 MW: 50360AAaPerleayrEP:64;			
alignment_scores:				
	Quality: 825.50	Length: 188		
	Ratio: 5.064	Gaps: 1		
	Percent Similarity: 86.762	Percent Identity: 78.191		
alignment_block:				
097530	265	342A	189	57330
Align seq 1/1 to: 097530 from: 1 to: 189				
1	ATGCGGCTTCGACGCTGGCTGCACCTGCTGGCTGCTGGCTGGCA	50		
?	MetGlycLeuThrValProGlyLeuLeuLeuLeuLeuLeuLeuLeu	17		
54	CGTGGGCT			


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seq_document at ion_block:
ID 000280 PRELIMINARY: PRI: 380 AA.
AC 000280:
DI 01-JUL-1997 (FEMHirel. 04, Created)
DT 01-JUL-1997 (FEMHirel. 04, Last sequence update)
DE 01-JUN-2001 (FEMHirel. 17, Last annotation update)
DE LYMPHOCTE ASSOCIATED RECEPTOR OF DEATH 9.
OS Homo sapiens (Human).
OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
OC Mammalia, Eutheria, Primates, Catarrhini, Hominoidea, Homo.
OX NCBI_TaxID=9606;
RN 111
RP SEQUENCE FROM N.A.
RX MEDLINE=9727273; PubMed 9114039;
RA Sreteron G.E., Xu X.N., Olsen A.L., Cowper A.E., Tan R.,
RA McMichael A.J., Bell J.L.;
RT "IAPs: a new lymphoid-specific death domain containing receptor
RT regulated by alternative pre-mRNA splicing.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
DR EMBL: U94510; AAC51315.1;
DR HSSP: P19438; TEXT;
DR InterPro: IPR000488; Death;
DR InterPro: IPR000561; EGF-like;
DR InterPro: IPR001368; TNFR_c6;
DR Pfam: PF00531; death_1;
DR SMART: SM00005; DEATH_1;
DR SMART: SM00208; TNFR_2;
DR PROSITE: PS00017; DEATH_DOMAIN; 1;
DR PROSITE: PS01186; EGF_2; UNKNOWN_1;
DR PROSITE: PS00652; TNFR_NGFR_1; 2;
DR PROSITE: PS00652; TNFR_NGFR_2; 1;
SQ SEQUENCE 380 AA: 41192 MW: 80194586.60094787 CRC64;

alignment_scores:
Quality: 209.50 Length: 186
Ratio: 2.054 Gaps: 7
Percent Similarity: 54.839 Percent Identity: 29.032

US-09-525-998a-11 x 000280

Align seq 1/1 to: 000280 from: 1 to: 380

43 CTCCTGGAGCTGTGGTGGGAATATATACCCCTCAGGGGTATATGGCAATAG 92
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
15 LeuLeuLeuValLeuLeuLeuGlyAlaArgAlaGlyGlyGlyThrArgSerPr 31
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
93 TCTGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 142
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
31 oargCysaspCysAlaGlyAspThrHisTyrGlyGlyGlyGlyGlyGlyGly 48
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
143 GTATATATATATATATATATATATATATATATATATATATATATATAT 192
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48 ysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysIhrGluPro 64
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
193 GGGAGGATATACGACATGACGACATGACGACGACGACGACGACGACGACG 242
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
65 CysGlyAsnSerThrCysLeuValCysProGluAspThrPheLeuAlaTr 81
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
243 ACAAAACACCTCACA...CATTCCTCAGCTCTGCAATATGCCAAAGC 289
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
81 pGluAsnHisHisAsnSerThrCysAlaArgCysGlnAlaCysAspGlu 99
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
260 AANTGATATATATATATATATATATATATATATATATATATATATATAT 339
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
98 InAlaSerGlnValAlaLeuGluAsnGlySerAlaValAlaAspThrArg 114
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
340 TGTGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 142
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
115 CysGlyTyrSerProGlyTyrPheValSerCysGlyGlyGlyGlyGlyGly 192

```


DT 01-MAY-2000 (TREMREL: 13, Last sequence update)
 DT 01-JUN-2001 (TREMREL: 17, Last annotation update)
 DE LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 4.
 OS Homo sapiens (Human)
 OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
 CC Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97272223; PubMed=9114039;
 RA Scragton G.R., Xu X.N., Olsen A.L., Cowper A.E., Tan R.,
 RA McMichael A.J., Bell J.I.;
 RT "LARD: a new lymphoid-specific death domain containing receptor
 RT regulated by alternative pre-mRNA splicing."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
 DR EMBL: U94505; AAC51310.1; -;
 DR HSP: P19438; IEXT.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 2.
 DR SMART: SM00208; INFR; 2.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS00050; TNFR_NGFR_2; 1.
 KW Receptor.
 SQ SEQUENCE 161 AA; 14432 MW; 59AAFE0BB846F664 CRC64;

alignment_scores:

Quality: 205.00 Length: 168
 Ratio: 2.204 Gaps: 5
 Percent Similarity: 55.357 Percent Identity: 30.357

alignment_block:

US-09-525-998A-11 x Q90M61

Align seq 1/1 to: Q90M61 from: 1 to: 181

43 GTCCGCGAGCGTGGTGGGATATACGCGGATATGGAGATAG 92
 15 LeuLeuLeuValLeuLeuGlyValArgAlaGlnGlyGlyThrArgSerPr 31
 93 TGT 142
 31 oArgCysAspCysAlaGlyAspPheHisLysLysLysLysLys 48
 143 GTACCAAGTGTGCACAAAGCAACCTACTCTGACAAAGACGTC 192
 48 ysArgGlyCysProAlaGlyHisThrLeuLysAlaProCysThrGluPro 64
 193 GGGGAGGATACGACATACAGGAGAGAGAGAGAGAGAGAGAG 242
 65 CysGlyAsnSerThrCysLeuValCysProGlnAspThrLeuAlaTr 81
 243 AAAAAAATAATATAAATAATATAATATAATATAATATAATATA 289
 81 pGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluG 98
 290 AAAAGGGGACGTGGAGATGCTCTCTCTCTCTCTCTCTCTCT 339
 98 InAlaSerGluValAlaLeuGluAsnGlySerAlaValAlaAspThrArg 114
 340 TGTGCTGCACAGACACACACACACACACACACACACACACAC 389
 115 CysGlyCysLysProGlyThrPheValCysGlnValSer 128
 390 rCAspGln 134
 128 rClnCysValSerSerProPheThrCysGlnProCysLysCysG 145
 422 GCACCGTGCACACACACACACACACACACACACACACACAC 459
 145 lyAlaLeuHisArgHisThrArgLeuLeuLeuLeuLeuLeuLeu 161

460 GGTGGATCTGCAATGAGGTTTCTTCTTCTTCTTCTTCTTCT 509
 162 CysGlyThrCysLeuProCysGlyPheCysHisSerGlyAspGly 178
 510 CTGT 513
 178 rCys 179

seq_name: sp_fodent_0920W1

seq_documentation_block:

ID Q920W1 PBLIMINARY: PRT: 417 AA.
 AC Q920W1;
 DT 01-MAY-1999 (TREMREL: 10, Created)
 DT 01-MAY-1999 (TREMREL: 10, Last sequence update)
 DT 01-JUN-2001 (TREMREL: 17, Last annotation update)
 DE NERVE GROWTH FACTOR RECEPTOR.
 OS Mus musculus (Mouse).
 CC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
 CC Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN A;
 PX MEDLINE=94077753; PubMed=9257182;
 RA Tuffereau C., Hennequin J., Blondel D., Kieffer H., Flamanet A.;
 RT "Low-affinity nerve-growth factor receptor (p75NTR) can serve as a
 RT receptor for rabies virus."
 RL EMBL: J. 17:259-259(1998).
 DR EMBL: AF105292; AAC17943.1; -;
 DR RSP: F07174; INGR.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000734; Lipase.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00531; Death; 1.
 DR Pfam: PF00020; TNFR_c6; 4.
 DR Pfam: PF00020; TNFR_c6; 1.
 DR SMART: SM00208; INFR; 3.
 DR PROSITE: PS00017; DEATH_DOMAIN; 1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE: PS00120; LIPASE_SER; UNKNOWN_1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS00050; TNFR_NGFR_2; 4.
 KW Receptor.
 SQ SEQUENCE 417 AA; 44686 MW; 5D7A4510B8A19B2 CRC64;

alignment_scores:

Quality: 204.50 Length: 198
 Ratio: 1.859 Gaps: 12
 Percent Similarity: 55.556 Percent Identity: 31.818

alignment_block:

US-09-525-998A-11 x Q920W1

Align seq 1/1 to: Q920W1 from: 1 to: 417

22 GATCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 71
 2 AsnArgLeuArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 18
 72 CTACAGGCGCTATACCAATACATGCTGTGTGTGTGTGTGTGTGT 121
 18 eGlyGly.....AlaLysLeuThrCysSerThrGlyMetThrHis 32
 122 CTCAATAATATGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 171
 33SerCysCysCysLysAlaCysLeuGlyGlyVal 46
 172 TAT 219

